

FIG. 1

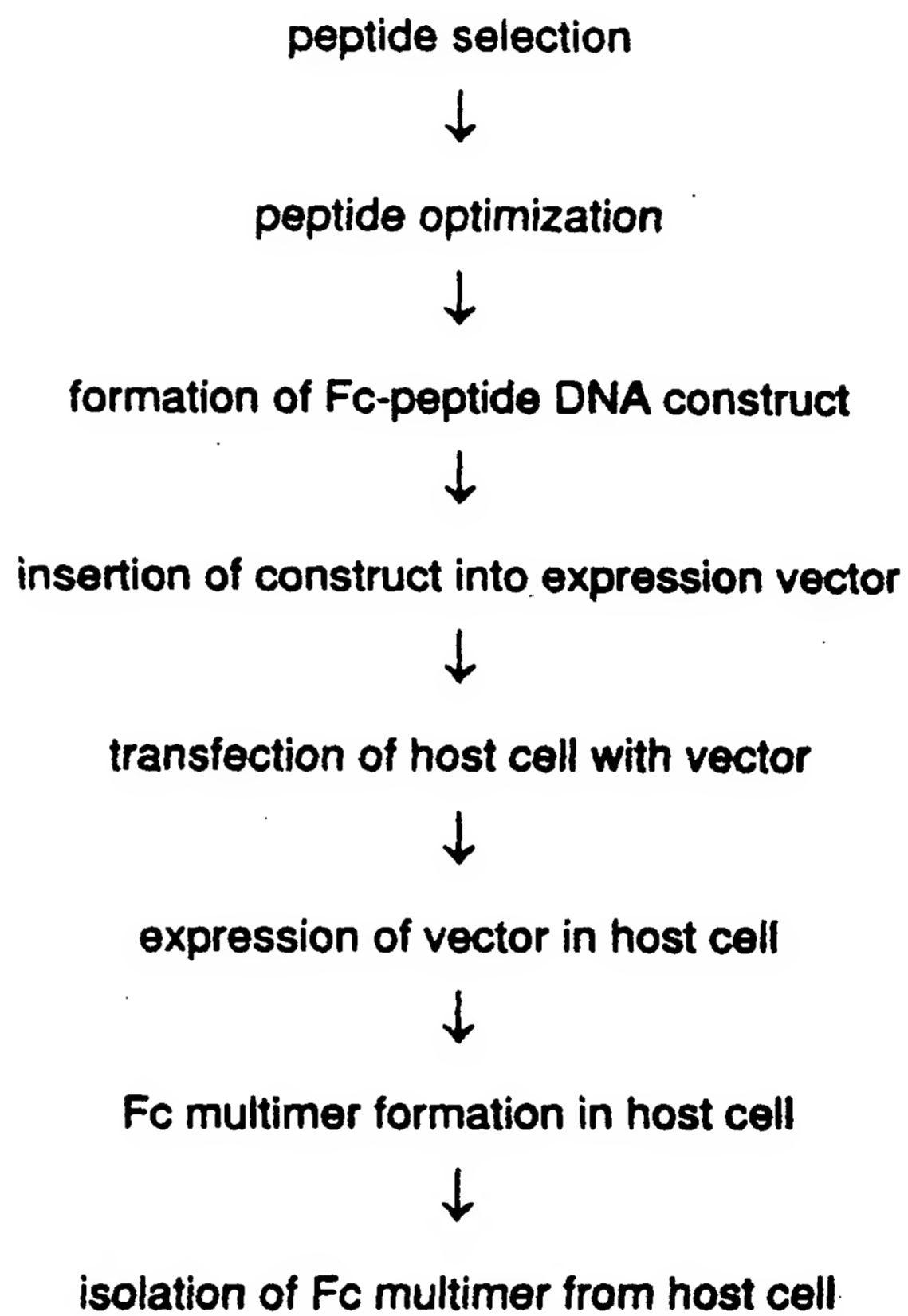


FIG. 2A

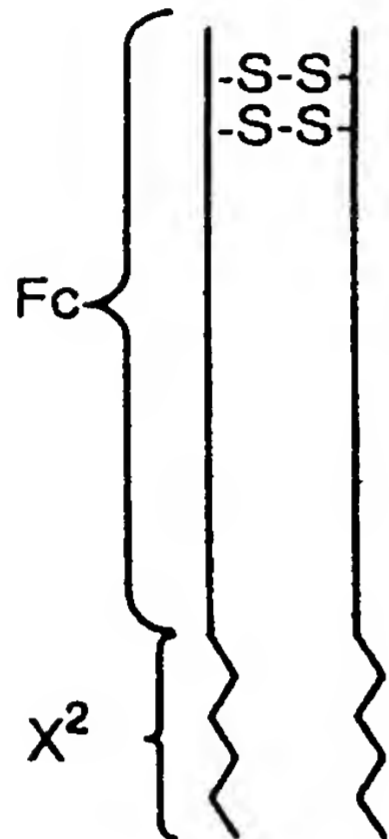


FIG. 2B

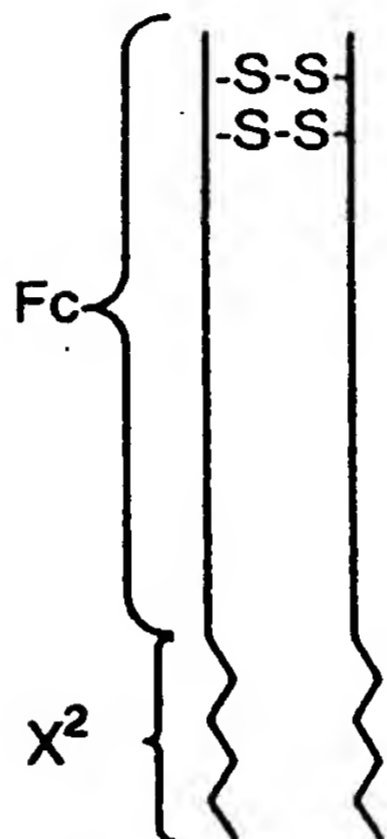


FIG. 2C

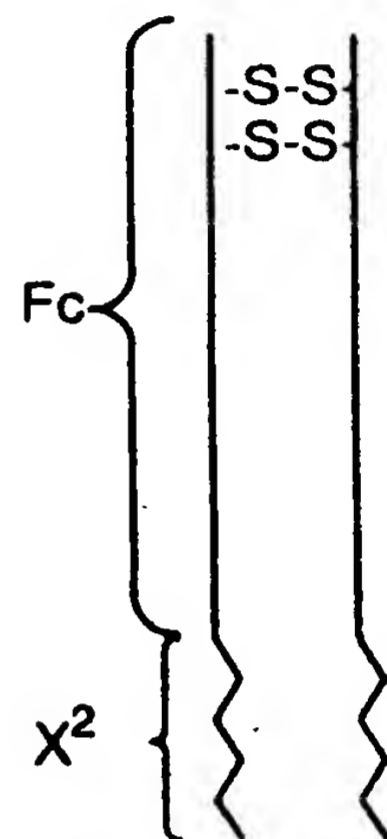


FIG. 2D

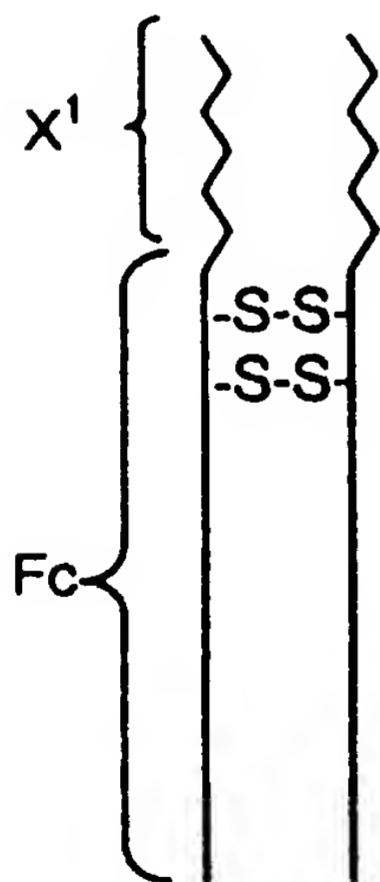


FIG. 2E

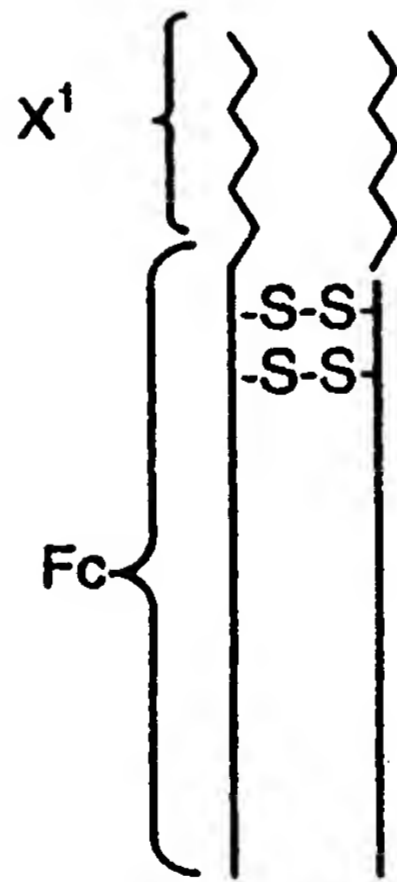


FIG. 2F

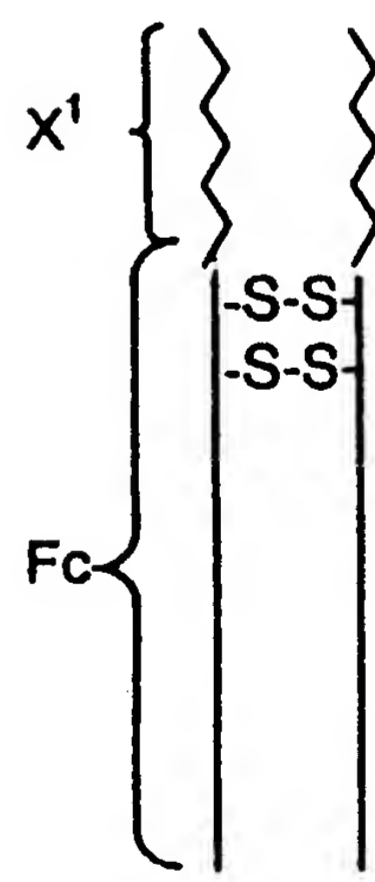


FIG. 3A

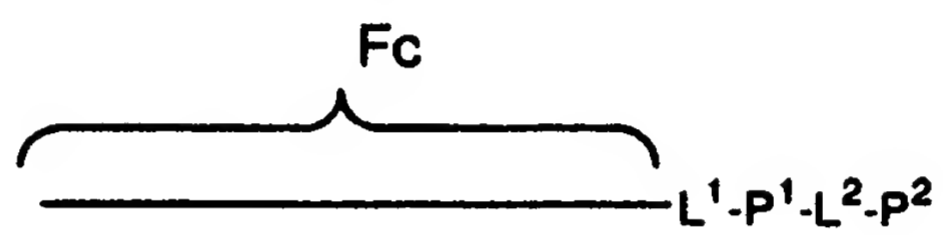


FIG. 3B

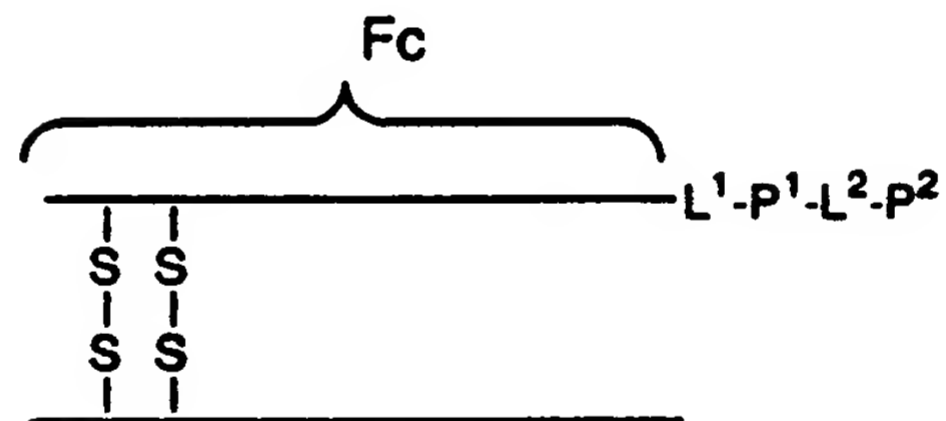


FIG. 3C

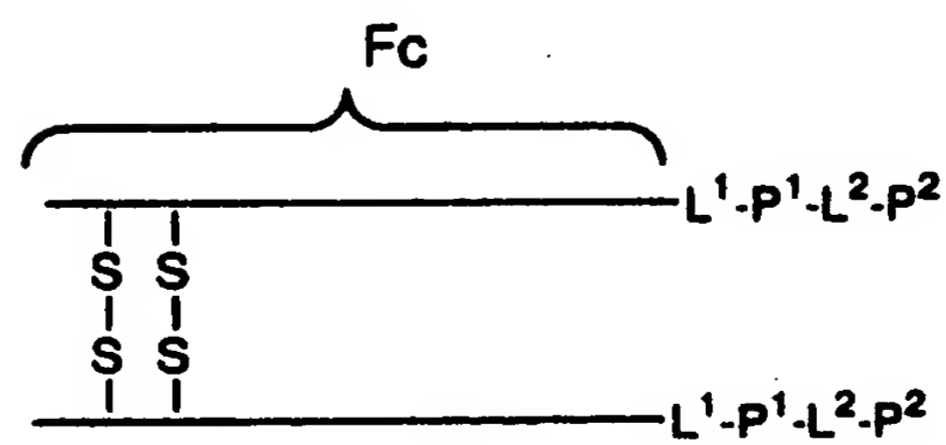


FIG. 4

ATGGACAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCCTGGGGGGACCGTCA
1 -----+-----+-----+-----+-----+-----+-----+ 60
TACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGT
a M D K T H T C P P C P A P E L L G G P S -
GTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC
61 -----+-----+-----+-----+-----+-----+ 120
CAGAAGGAGAAGGGGGGTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAG
a V F L F P P K P K D T L M I S R T P E V -
ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
121 -----+-----+-----+-----+-----+-----+ 180
TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC
a T C V V V D V S H E D P E V K F N W Y V -
GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
181 -----+-----+-----+-----+-----+-----+ 240
CTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGC
a D G V E V H N A K T K P R E E Q Y N S T -
TACCGTGTGGTCAGCGTCCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
241 -----+-----+-----+-----+-----+-----+ 300
ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATG
a Y R V V S V L T V L H Q D W L N G K E Y -
AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGCC
301 -----+-----+-----+-----+-----+-----+ 360
TTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGG
a K C K V S N K A L P A P I E K T I S K A -
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC
361 -----+-----+-----+-----+-----+-----+ 420
TTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGG
a K G Q P R E P Q V Y T L P P S R D E L T -
AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG
421 -----+-----+-----+-----+-----+-----+ 480
TTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC
a K N Q V S L T C L V K G F Y P S D I A V -
GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCTGGAC
481 -----+-----+-----+-----+-----+-----+ 540
CTCACCTCTCGTTACCCGTGCGCCTCTTGTGTGATGTTCTGGTGCGGAGGGCACGACCTG
a E W E S N G Q P E N N Y K T T P P V L D -
TCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
541 -----+-----+-----+-----+-----+-----+ 600
AGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTC
a S D G S F F L Y S K L T V D K S R W Q Q -
GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG
601 -----+-----+-----+-----+-----+-----+ 660
CCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTC
a G N V F S C S V M H E A L H N H Y T Q K -
AGCCTCTCCCTGTCTCCGGGTAAA
661 -----+-----+-----+-----+-----+ 684
TCGGAGAGGGACAGAGGCCCATTT

FIG. 5

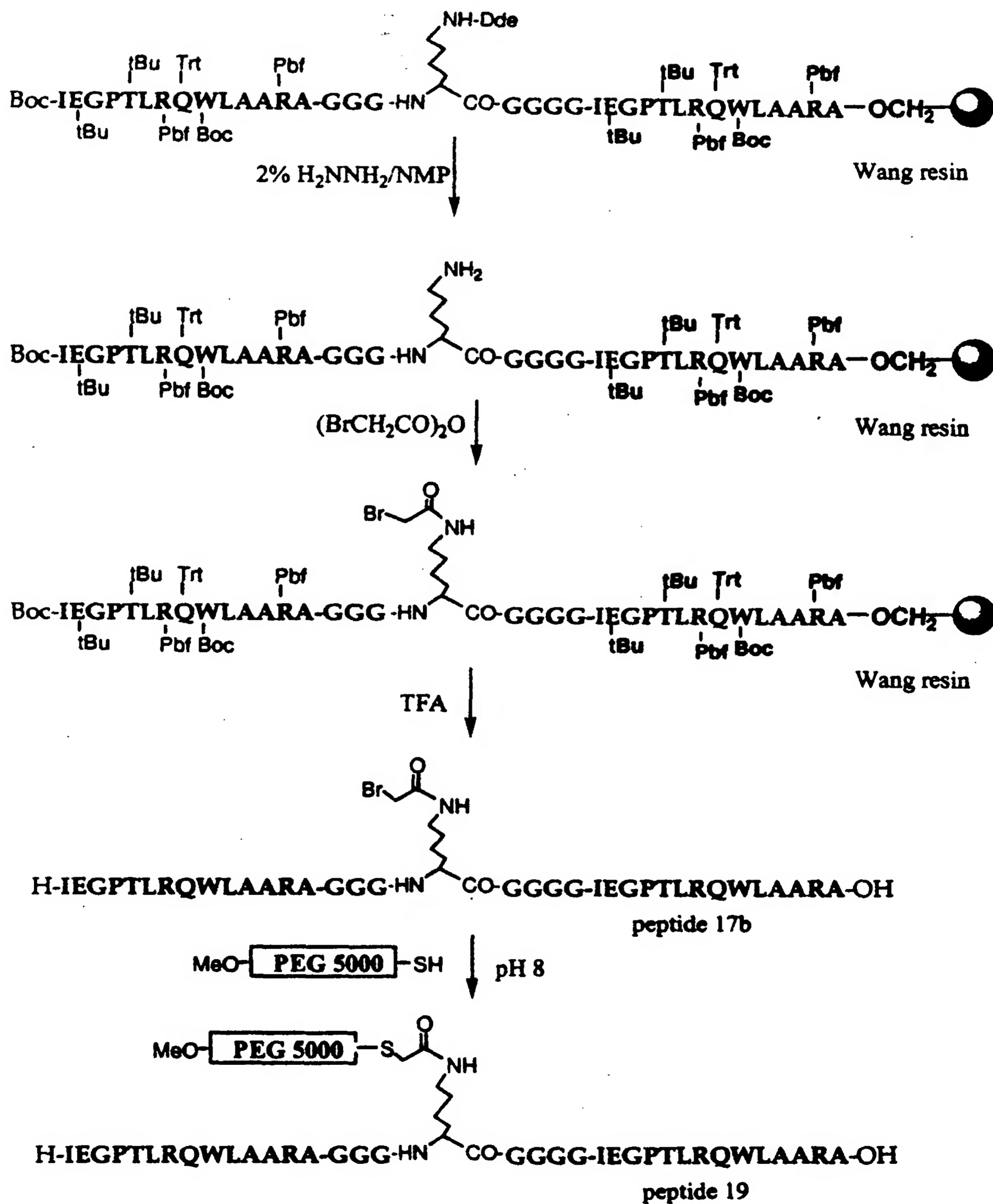


FIG. 6

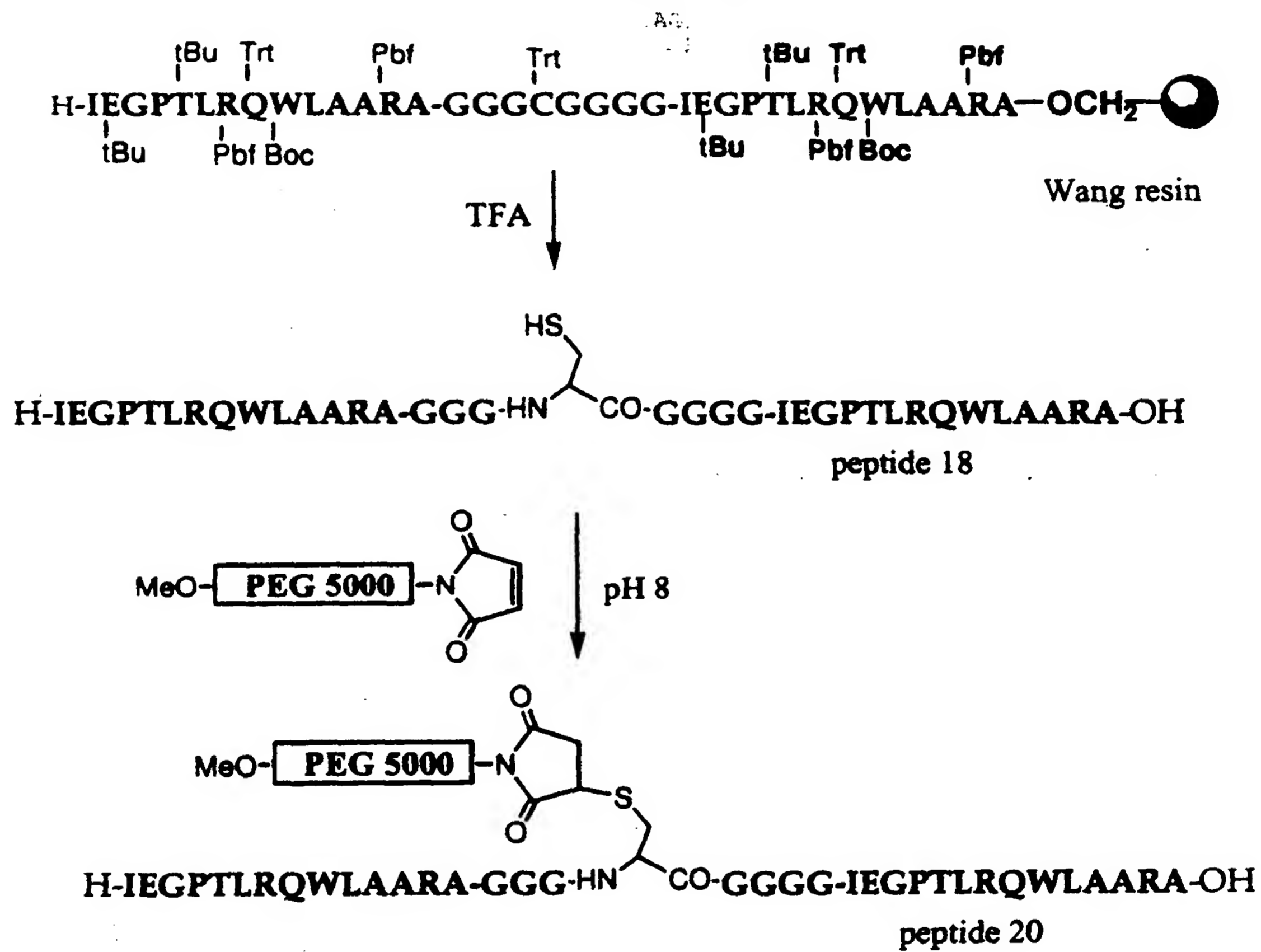


FIG. 8

XbaI
|
1 TCTAGATTTGTTTAACTAATTAAAGGAGGAATAACATATGGACAAACTCACACATGTC 60
AGATCTAAACAAAATTGATTAATTCCTCCTTATTGTATACCTGTTTTGAGTGTGTACAG
M D K T H T C P
61 CACCTTGTCCAGCTCCGGAACCTCGGGGGACCGTCAGTCTTCCTCTTCCCCCAAAC 120
GTGGAACAGGTGAGGCCTTGAGGACCCCTGGCAGTCAGAAGGAGAAGGGGGTTTTG
P C P A P E L L G G P S V F L F P P K P
121 CCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGA 180
GGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT
K D T L M I S R T P E V T C V V V D V S
181 GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG 240
CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
H E D P E V K F N W Y V D G V E V H N A
241 CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCA 300
GGTTCCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGT
K T K P R E E Q Y N S T Y R V V S V L T
301 CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAG 360
GGCAGGACGTGGTCTGACCGACTTACCGTTCTCATGTTTCACGTTCCAGAGGTTGTTTC
V L H Q D W L N G K E Y K C K V S N K A
361 CCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC 420
GGGAGGGTCCGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG
L P A P I E K T I S K A K G Q P R E P Q
421 AGGTGTACACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT 480
TCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGGTTCCTGGTCCAGTCGGACTGGA
V Y T L P P S R D E L T K N Q V S L T C
481 GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC 540
CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCG
L V K G F Y P S D I A V E W E S N G Q P
541 CGGAGAACAACACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTCCTCT 600
GCCTCTTGTTGATGTTCTGGTGGGAGGGACGACCTGAGGCTGCCGAGGAAGAAGGAGA
E N N Y K T T P P V L D S D G S F F L Y
601 ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG 660
TGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGCAGAAGAGTACGAGGC
S K L T V D K S R W Q Q G N V F S C S V
661 TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA 720
ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT
M H E A L H N H Y T Q K S L S L S P G K
721 AAGGTGGAGGTGGTGGTATCGAAGGTCCGACTCTGCGTCAGTGGCTGGCTGCTCGTGCTG 780
TTCCACCTCCACCACCATAGCTTCCAGGCTGAGACGCAGTCACCGACCGACGAGCACGAC
G G G G G I E G P T L R Q W L A A R A G
781 GTGGTGGAGGTGGCGGCGGAGGTATTGAGGGCCCAACCCTTCGCCAATGGCTTGCAGCAC 840
CACCACCTCCACCGCCGCTCCATAACTCCCGGGTTGGGAAGCGGTTACCGAACGTCGTG
G G G G G G I E G P T L R Q W L A A R
BamHI
|
841 GCGCATAATCTCGAGGATCCG 861
CGCGTATTAGAGCTCCTAGGC
A * -

BamHI
|
GTAAATAATGGATCC
841+..... 855
CATTATTACCTAGG
K *

FIG. 10

XbaI
|
1 TCTAGATTGTTTAACTAATTAAGGAGGAATAACATATGATCGAAGGTCCGACTCTGC 60
.....+.....+.....+.....+.....+.....+.....+.....+.....+
AGATCTAAACAAAATTGATTAATTCCTCCTTATTGTATACTAGCTTCCAGGCTGAGACG
M I E G P T L R

61 GTCAGTGGCTGGCTGCTCGTGCTGGTGGAGGCGGTGGGGACAAACTCACACATGTCCAC 120
.....+.....+.....+.....+.....+.....+.....+.....+.....+
CAGTCACCGACCGACGAGCAGCACCACCTCCGCCACCCCTGTTTTGAGTGTGTACAGGTG
Q W L A A R A G G G G G D K T H T C P P

121 CTTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTTTTCCTCTTCCCCC AAAACCCA 180
.....+.....+.....+.....+.....+.....+.....+.....+.....+
GAACGGGTGCTGGACTTGAGGACCCCCCTGGCAGTCAAAGGAGAAGGGGGGTTTTGGGT
C P A P E L L G G P S V F L F P P K P K

181 AGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCC 240
.....+.....+.....+.....+.....+.....+.....+.....+.....+
TCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGG
D T L M I S R T P E V T C V V V D V S H

241 ACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCA 300
.....+.....+.....+.....+.....+.....+.....+.....+.....+
TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT
E D P E V K F N W Y V D G V E V H N A K

301 AGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCG 360
.....+.....+.....+.....+.....+.....+.....+.....+.....+
TCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGC
T K P R E E Q Y N S T Y R V V S V L T V

361 TCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC 420
.....+.....+.....+.....+.....+.....+.....+.....+.....+
AGGACGTGGTCTGACCGACTTACCGTTCTCATGTTACGTTCCAGAGGTTGTTTCGGG
L H Q D W L N G K E Y K C K V S N K A L

421 TCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG 480
.....+.....+.....+.....+.....+.....+.....+.....+.....+
AGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCC
P A P I E K T I S K A K G Q P R E P Q V

481 TGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCC 540
.....+.....+.....+.....+.....+.....+.....+.....+.....+
ACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCCTTGGTCCAGTCGGACTGGACGG
Y T L P P S R D E L T K N Q V S L T C L

541 TGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG 600
.....+.....+.....+.....+.....+.....+.....+.....+.....+
ACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCGGCC
V K G F Y P S D I A V E W E S N G Q P E

601 AGAACA ACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACA 660
.....+.....+.....+.....+.....+.....+.....+.....+.....+
TCTTGTGATGTTCTGGTGCAGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGT
N N Y K T T P P V L D S D G S F F L Y S

661 GCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGA 720
.....+.....+.....+.....+.....+.....+.....+.....+.....+
CGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAAGAAGTACGAGGCACT
K L T V D K S R W Q Q G N V F S C S V M

721 TGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCGGGTAAAT 780
.....+.....+.....+.....+.....+.....+.....+.....+.....+
ACGTACTCCGAGACGTGTTGGTGTATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTA
H E A L H N H Y T Q K S L S L S P G K *

BamHI
|
781 AATGGATCC 789
TTACCTAGG

FIG.11

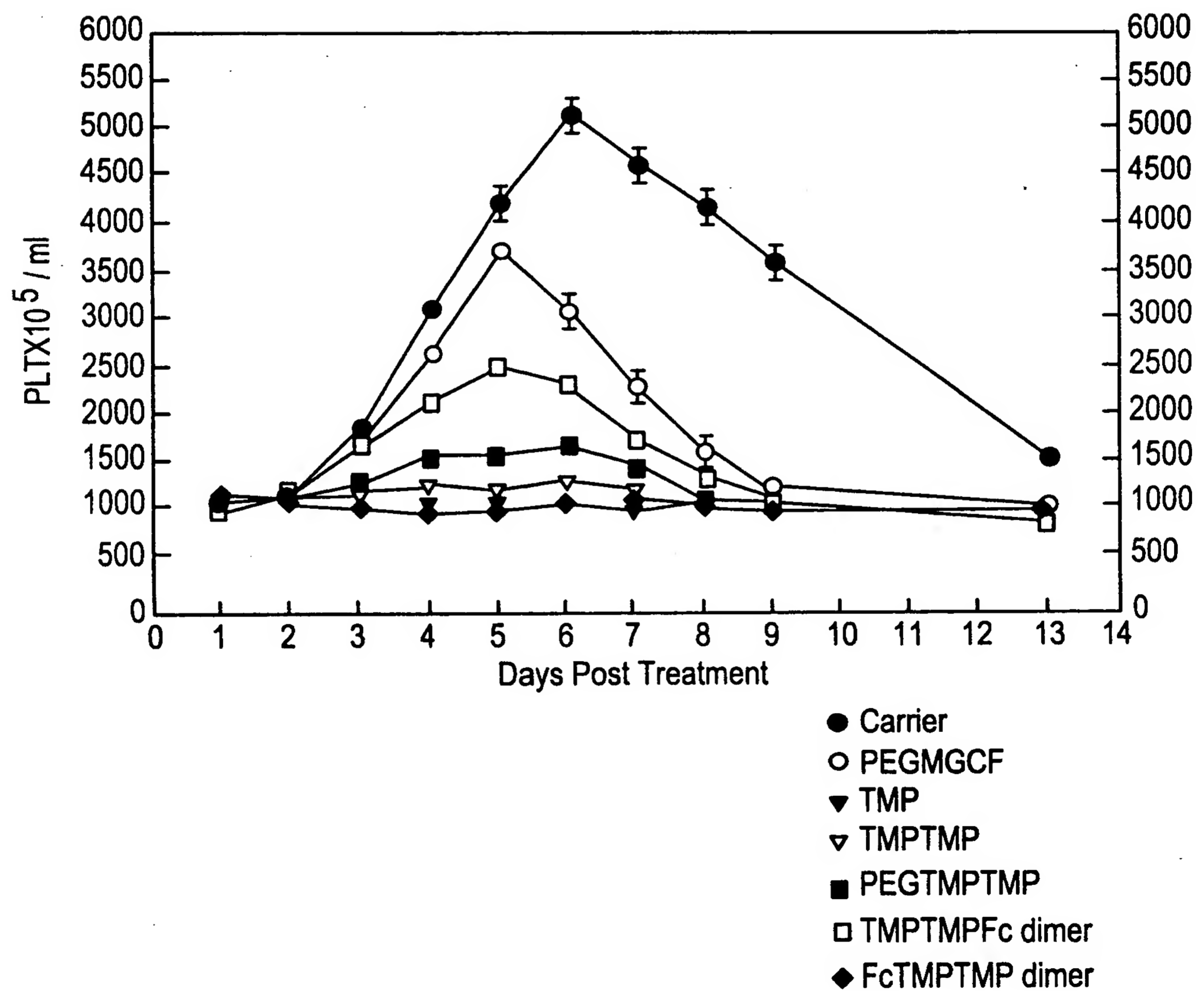


FIG.12

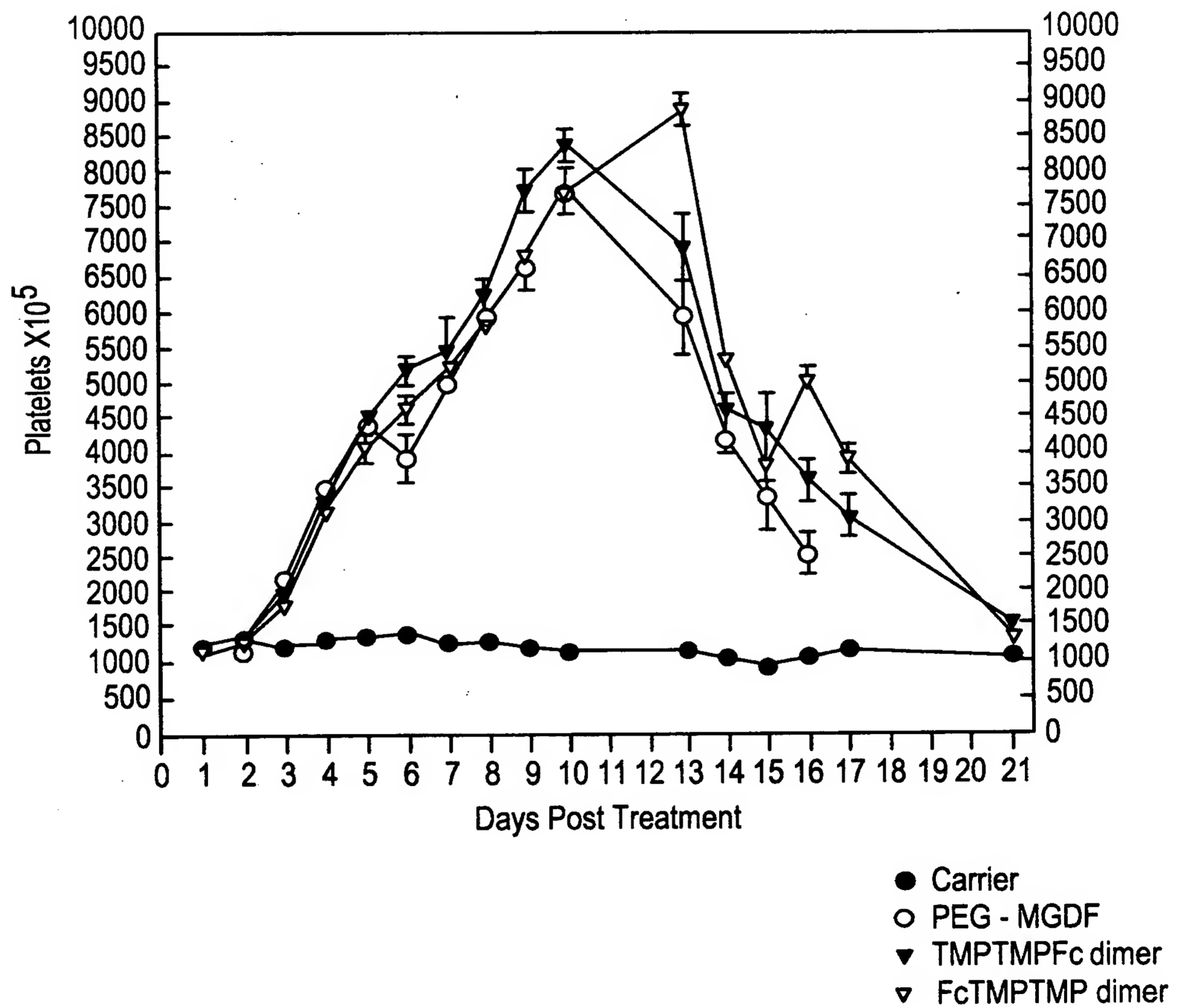


FIG. 13

XbaI
|

1 TCTAGATTGTTTAACTAATTAAGGAGGAATAACATATGGACAAACTCACACATGTC 60
.....+.....+.....+.....+.....+.....+.....+.....+.....+ 60
AGATCTAAACAAAATTGATTAATTTCTCTCTTATTGTATACCTGTTTTGAGTGTGTACAG
CACCTTGTCCAGCTCCGGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAC
61+.....+.....+.....+.....+.....+.....+.....+.....+ 120
GTGGAACAGGTGAGGCCCTTGAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTG
P C P A P E L L G G P S V F L F P P K P
CCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGA
121+.....+.....+.....+.....+.....+.....+.....+.....+ 180
GGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT
K D T L M I S R T P E V T C V V V D V S
GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
181+.....+.....+.....+.....+.....+.....+.....+.....+ 240
CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
H E D P E V K F N W Y V D G V E V H N A
CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCA
241+.....+.....+.....+.....+.....+.....+.....+.....+ 300
GGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGT
K T K P R E E Q Y N S T Y R V V S V L T
CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
301+.....+.....+.....+.....+.....+.....+.....+.....+ 360
GGCAGGACGTGGTCTGACCGACTTACCGTTCTCTCATGTTTACGTTCCAGAGGTTGTTTC
V L H Q D W L N G K E Y K C K V S N K A
CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCAC
361+.....+.....+.....+.....+.....+.....+.....+.....+ 420
GGGAGGGTTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG
L P A P I E K T I S K A K G Q P R E P Q
AGGTGTACACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTACGCCTGACCT
421+.....+.....+.....+.....+.....+.....+.....+.....+ 480
TCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGA
V Y T L P P S R D E L T K N Q V S L T C
GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
481+.....+.....+.....+.....+.....+.....+.....+.....+ 540
CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCG
L V K G F Y P S D I A V E W E S N G Q P
CGGAGAACAACACTACAAGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCT
541+.....+.....+.....+.....+.....+.....+.....+.....+ 600
GCCTCTTGTGATGTTCTGGTGGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGA
E N N Y K T T P P V L D S D G S F F L Y
ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG
601+.....+.....+.....+.....+.....+.....+.....+.....+ 660
TGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAAGAGTACGAGGC
S K L T V D K S R W Q Q G N V F S C S V
TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA
661+.....+.....+.....+.....+.....+.....+.....+.....+ 720
ACTACGTACTCCGAGACGTGTTGGTGTATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT
M H E A L H N H Y T Q K S L S L S P G K
AAGGTGGAGGTGGTGGTGGAGGTACTTACTCTTGCCACTTCGGCCCGCTGACTTGGGTTT
721+.....+.....+.....+.....+.....+.....+.....+.....+ 780
TTCCACCTCCACCACCACCTCCATGAATGAGAACGGTGAAGCCGGGCGACTGAACCCAAA
G G G G G G G T Y S C H F G P L T W V C
BamHI
|

781 GCAAACCGCAGGGTGGTTAATCTCGTGGATCC 812
CGTTTGGCGTCCCACCAATTAGAGCACCTAGG
K P Q G G *

FIG. 14

XbaI
|
TCTAGATTGTTTAACTAATTAAAGGAGGAATAACATATGGGAGGTACTTACTCTTGCC
1+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 60
AGATCTAAACAAAATTGATTAATTCCTCCTTATTGTATACCCTCCATGAATGAGAACGG
M G G T Y S C H -
c
ACTTCGGCCCCGCTGACTTGGGTATGTAAGCCACAAGGGGGTGGGGGAGGCGGGGGGACA
61+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 120
TGAAGCCGGGCGACTGAACCCATACATTGGGTGTTCCCCCACCCTCCGCCCCCCTGT
F G P L T W V C K P Q G G G G G G G G D K -
c
AAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGACCGTCAGTTTTC
121+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 180
TTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCTGGCAGTCAAAGG
T H T C P P C P A P E L L G G P S V F L -
c
TCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCG
181+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 240
AGAAGGGGGGTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGC
F P P K P K D T L M I S R T P E V T C V -
c
TGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG
241+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 300
ACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCCG
V V D V S H E D P E V K F N W Y V D G V -
c
TGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG
301+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 360
ACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCAC
E V H N A K T K P R E E Q Y N S T Y R V -
c
TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCA
361+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 420
ACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTACGT
V S V L T V L H Q D W L N G K E Y K C K -
c
AGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGC
421+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 480
TCCAGAGGTTGTTTCGGGAGGGTCCGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCG
V S N K A L P A P I E K T I S K A K G Q -
c
AGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACC
481+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 540
TCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGG
P R E P Q V Y T L P P S R D E L T K N Q -
c
AGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGG
541+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 600
TCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTGGCTGTAGCGGCACCTCACCC
V S L T C L V K G F Y P S D I A V E W E -
c
AGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCTCCCGTGCTGGACTCCGACG
601+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 660
TCTCGTTACCCGTCGGCCTCTTGTGTGATGTTCTGGTGGGAGGGCAGGACCTGAGGCTGC
S N G Q P E N N Y K T T P P V L D S D G -
c
GCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACG
661+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 720
CGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGC
S F F L Y S K L T V D K S R W Q Q G N V -
c
TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT
721+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 780
AGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGTGATGTGCGTCTTCTCGGAGA
F S C S V M H E A L H N H Y T Q K S L S -
c
BamHI
|
CCCTGTCTCCGGGTAAATAATGGATCC
781+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 807
GGGACAGAGGCCCATTTATTACCTAGG
L S P G K *

FIG. 15

841 GCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC 881
+.....+.....+.....+
 CGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG
 O K S L S L S P G K *

FIG. 16

FIG. 16

XbaI

1 TCTAGATTGTGTTTAACTAATTAAGGAGGAATAACATATGGACAAACTCACACATGTC 60
.....+.....+.....+.....+.....+.....+.....+.....+.....+ 60
AGATCTAAACAAATTGATTAATTTCTCCTTATTGTATACCTGTTTGTAGTGTGTACAG
M D K T H T C P

61 CACCTTGCCCAGCACCTGAACTCCTGGGGGACCGTCAGTTTCTCTTCCCCCAAAC 120
.....+.....+.....+.....+.....+.....+.....+.....+.....+ 120
GTGGAACGGGTGCTGGACTTGAGGACCCCCCTGGCAGTCAAAAGGAGAAGGGGGGTTTTG
P C P T A P E L L G G P S V F L F P P K P

121 CCAAGGACACCCCTCATGATCTCCCGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA 180
.....+.....+.....+.....+.....+.....+.....+.....+.....+ 180
GGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT
K D T L M I S R T P E V T C V V V D V S

181 GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG 240
.....+.....+.....+.....+.....+.....+.....+.....+.....+ 240
CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
H E D P E V K F N W Y V D G V E V H N A

241 CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCA 300
.....+.....+.....+.....+.....+.....+.....+.....+.....+ 300
GGTTCGTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGT
K T K P R E E Q Y N S T Y R V V S V L T

301 CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG 360
.....+.....+.....+.....+.....+.....+.....+.....+.....+ 360
GGCAGGACGTGGTCTGACCGACTTACCGTTCCTCATGTTACGTTCCAGAGGTTGTTTC
V L H Q D W L N G K E Y K C K V S N K A

361 CCCTCCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC 420
.....+.....+.....+.....+.....+.....+.....+.....+.....+ 420
GGGAGGGTTCGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG
L P A P I E K T I S K A K G Q P R E P Q

421 AGGTGTACACCCTGCCTCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCT 480
.....+.....+.....+.....+.....+.....+.....+.....+.....+ 480
TCCACATGTGGGACGGAGGTAGGGCCCTACTCGACTGGTTCCTTGGTCCAGTCGGACTGGA
V Y T L P P S R D E L T K N Q V S L T C

481 GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC 540
.....+.....+.....+.....+.....+.....+.....+.....+.....+ 540
CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCG
L V K G F Y P S D I A V E W E S N G Q P

541 CGGAGAACAACACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCT 600
.....+.....+.....+.....+.....+.....+.....+.....+.....+ 600
GCCTCTTGTGATGTTCTGGTGGGAGGGCAGACCTGAGGCTGCCGAGGAAGAAGGAGA
E N N Y K T T P P V L D S D G S F F L Y

601 ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG 660
.....+.....+.....+.....+.....+.....+.....+.....+.....+ 660
TGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC
S K L T V D K S R W Q Q G N V F S C S V

661 TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA 720
.....+.....+.....+.....+.....+.....+.....+.....+.....+ 720
ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT
M H E A L H N H Y T Q K S L S L S P G K

721 AAGGTGGAGGTGGTGGCGGAGGTACTTACTCTTGCCACTTCGGCCCACTGACTTGGGTTT 780
.....+.....+.....+.....+.....+.....+.....+.....+.....+ 780
TTCCACCTCCACCACCGCTCCATGAATGAGAACGGTGAAGCCGGGTGACTGAACCCAAA
G G G G G G G T Y S C H F G P L T W V C

781 GCAAACCGCAGGGTGGCGGGCGGCGGCGGCGGTGGTACCTATTCTGTCAATTTGGCCCCG 840
.....+.....+.....+.....+.....+.....+.....+.....+.....+ 840
CGTTTGGCGTCCCACCGCCGCGCGCGGCCACCATGGATAAGGACAGTAAACCGGGCG
K P Q G G G G G G G G T Y S C H F G P L

BamHI

841 TGACCTGGGTATGTAAGCCACAAGGGGGTTAATCTCGAGGATCC 884
.....+.....+.....+.....+.....+.....+.....+.....+.....+ 884
ACTGGACCCATACATTGGTGTTCCCCCAATTAGAGCTCCTAGG
T W V C K P Q G G *

FIG. 17A

[AatII sticky end] 5' GCGTAACGTATGCATGGTCTCC -
(position #4358 in pAMG21) 3' TGCACGCATTGCATACGTACCAGAGG -

-CCATGCGAGAGTAGGGAACTGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACT -
-GGTACGCTCTCATCCCTTGACGGTCCGTAGTTTATTTTGCTTTCCGAGTCAGCTTTCTGA -

-GGGCCTTTCGTTTTATCTGTTGTTTGTCTGGTGAACGCTCTCCTGAGTAGGACAAATCCGC -
-CCCGGAAAGCAAATAGACAACAACAGCCACTTGCGAGAGGACTCATCCTGTTTAGGCG -

-CGGGAGCGGATTTGAACGTTGCGAAGCAACGGCCCGGAGGGTGGCGGGCAGGACGCCCCG -
-GCCCTCGCCTAAACTTGCAACGCTTCGTTGCCGGGCTCCACCGCCCGTCTGCGGGCG -

-CATAACTGCCAGGCATCAAATTAAGCAGAAGGCCATCCTGACGGATGGCCTTTTTTGCGT -
-GTATTTGACGGTCCGTAGTTTAATTCGTCTTCCGGTAGGACTGCCTACCGGAAAAACGCA -

AatII

-TTCTACAAACTCTTTTGTTTATTTTTCTAAATACATTCAAATATGGACGTCGTACTTAAC -
-AAGATGTTTGAGAAAACAAATAAAAAGATTTATGTAAGTTTATACCTGCAGCATGAATTG -

-TTTTAAAGTATGGGCAATCAATTGCTCCTGTTAAAATTGCTTTAGAAATACTTTGGCAGC -
-AAAATTCATACCCGTTAGTTAACGAGGACAATTTTAACGAAATCTTTATGAAACCGTCG -

-GGTTTGTTGTATTGAGTTTCATTTGCGCATTGGTTAAATGGAAAGTGACCGTGCGCTTAC -
-CCAAACAACATAACTCAAAGTAAACGCGTAACCAATTTACCTTTCACTGGCACGCGAATG -

-TACAGCCTAATATTTTTGAAATATCCCAAGAGCTTTTTCTTCGCATGCCCACGCTAAAC -
-ATGTCGGATTATAAAAACCTTTATAGGGTTCTCGAAAAAGGAAGCGTACGGGTGCGATTTG -

-ATTCTTTTTCTCTTTTGGTTAAATCGTTGTTTGATTTATTATTGCTATATTTATTTTTT -
-TAAGAAAAAGAGAAAACCAATTTAGCAACAACTAAATAATAAACGATATAAATAAAAAG -

-GATAATTATCAACTAGAGAAGGAACAATTAATGGTATGTTTCATACACGCATGTAAAAATA -
-CTATTAATAGTTGATCTCTTCCTTGTTAATTACCATAACAAGTATGTGCGTACATTTTTAT -

-AACTATCTATATAGTTGTCTTTCTCTGAATGTGCAAACTAAGCATTCGGAAGCCATTAT -
-TTGATAGATATATCAACAGAAAGAGACTTACACGTTTTGATTTCGTAAGGCTTCGGTAATA -

-TAGCAGTATGAATAGGGAACTAAACCCAGTGATAAGACCTGATGATTTTCGCTTCTTTAA -
-ATCGTCATACTTATCCCTTTGATTTGGGTCACTATTCTGGACTACTAAAGCGAAGAAATT -

-TTACATTTGGAGATTTTTTTATTTACAGCATTGTTTTCAAATATATTCCAATTAATCGGTG -
-AATGTAAACCTCTAAAAATAAATGTCGTAACAAAAGTTTATATAAGGTTAATTAGCCAC -

-AATGATTGGAGTTAGAATAATCTACTATAGGATCATATTTTATTAAATTAGCGTCATCAT -
-TTACTAACCTCAATCTTATTAGATGATATCCTAGTATAAAATAATTTAATCGCAGTAGTA -

-AATATTGCCTCCATTTTTTTAGGGTAATTATCCAGAATTGAAATATCAGATTTAACCATAG -
-TTATAACGGAGGTAAAAAATCCCATTAATAGGTCTTAACCTTATAGTCTAAATTGGTATC -

-AATGAGGATAAATGATCGCGAGTAAATAATATTCACAATGTACCATTTTAGTCATATCAG -
-TTACTCCTATTTACTAGCGCTCATTTATTATAAGTGTTACATGGTAAATCAGTATAGTC -

-ATAAGCATTGATTAATATCATTATTGCTTCTACAGGCTTTAATTTTATTAATTATCTGT -
-TATTCGTAACCTAATTATAGTAATAACGAAGATGTCCGAAATTAATAATAATAAGACA -

-AAGTGTCGTCGGCATTATGTCTTTCATACCCATCTCTTTATCCTTACCTATTGTTTGTC -
-TTCACAGCAGCCGTAAATACAGAAAGTATGGGTAGAGAAATAGGAATGGATAACAAACAG -

-GCAAGTTTTGCGTGTTATATATCATTAACGCGTAATAGATTGACATTTGATTCTAATAA -
-CGTTCAAAACGCACAATATATAGTAATTTTGCCATTATCTAACTGTAAACTAAGATTATT -

FIG. 17B

- ATTGGATTTTGTGTCACACTATTATATCGCTTGAAATACAATTGTTTAAACATAAGTACCTG -
- TAACCTAAAAACAGTGTGATAATATAGCGAACTTTATGTTAACAAATTGTATTCATGGAC -
- TAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTATAGTCGATTAATCGATTTGATT -
- ATCCTAGCATGTCCAAATGCGTTCTTTTACCAAACAATATCAGCTAATTAGCTAAACTAA -
- CTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGA -
- GATCTAAACAAAATTGATTAATTCCTCCTTATTGTATACCAATTGCGCAACCTTAAGCT -
- GCTCACTAGTGTCGACCTGCAGGGTACCATGGAAGCTTACTCGAGGATCCGCGGAAAGAA -
- CGAGTGATCACAGCTGGACGTCCCATGGTACCTTCGAATGAGCTCCTAGGCGCCTTTCTT -
- GAAGAAGAAGAAGAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATA -
- CTTCTTCTTCTTCTTTCGGGCTTTCCTTCGACTCAACCGACGACGGTGGCGACTCGTTAT -
- ACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTTGCTGAAAGGAGG -
- TGATCGTATTGGGGAACCCCGGAGATTGCCCAGAACTCCCCAAAAACGACTTTCCTCC -
- AACCGCTCTTCACGCTCTTCACGC 3' [SacII sticky end]
- TTGGCGAGAAGTGCGAGAAGTG 5' (position #5904 in pAMG21)

FIG.18A - 1

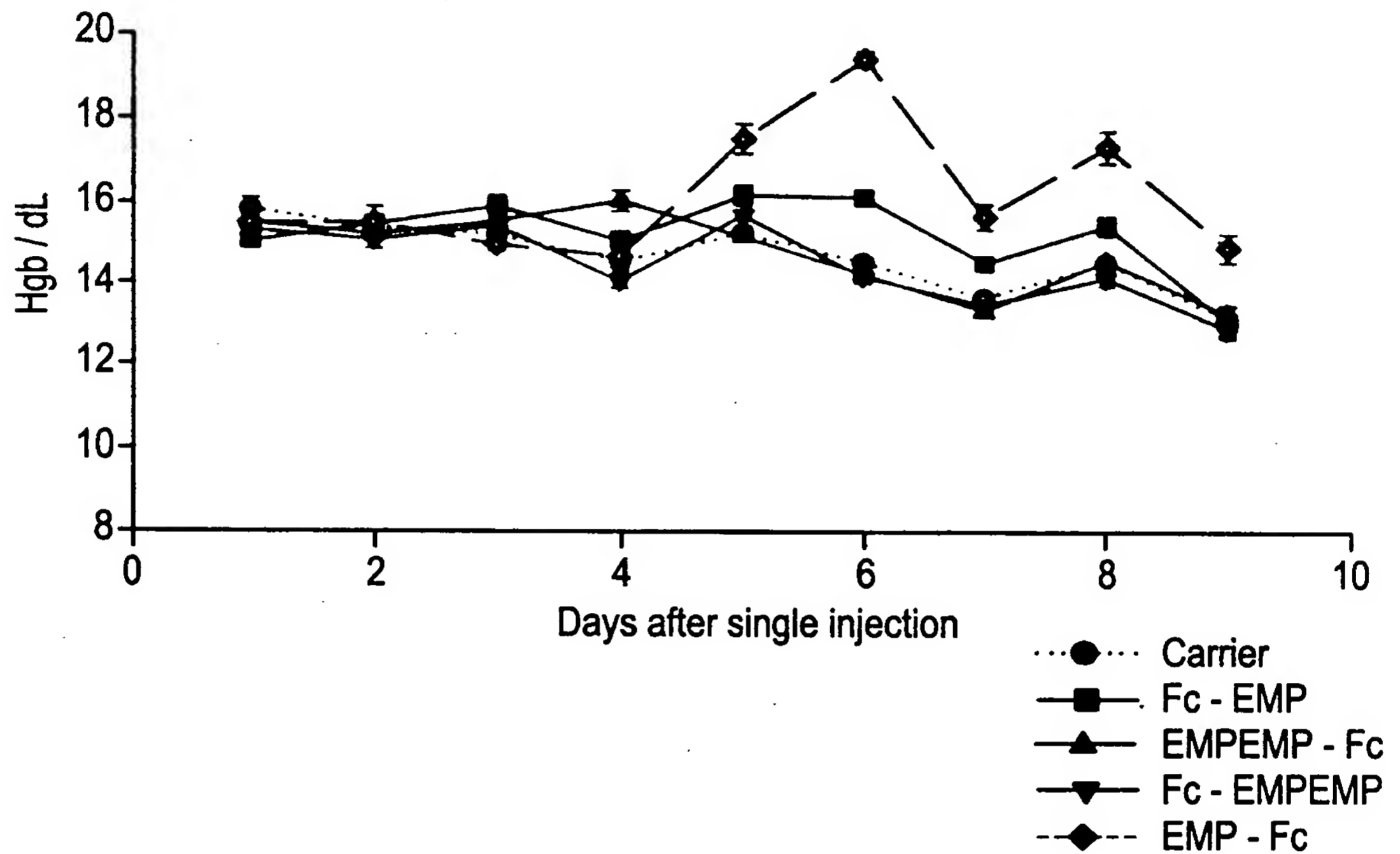


FIG.18A - 2

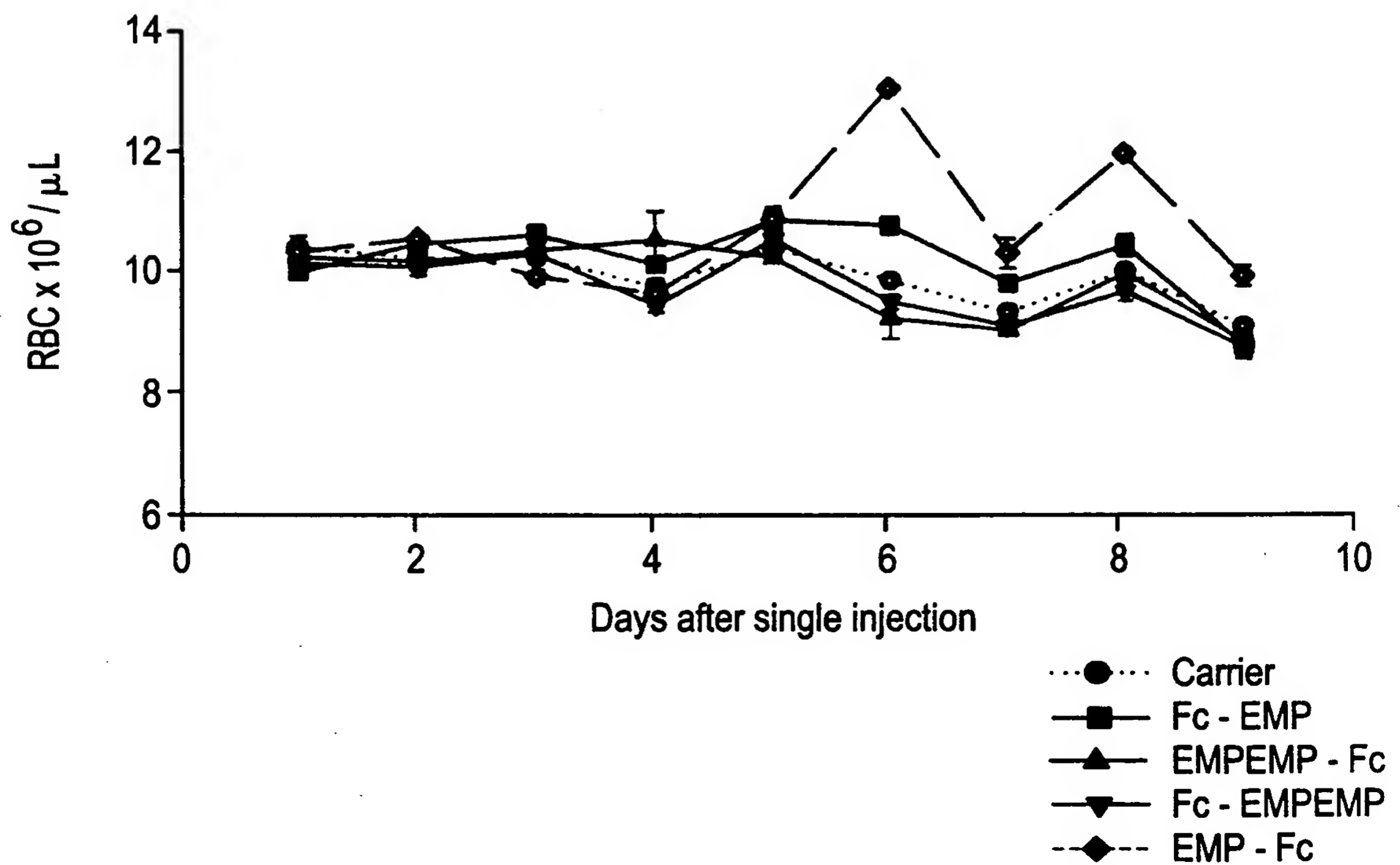


FIG.18A - 3

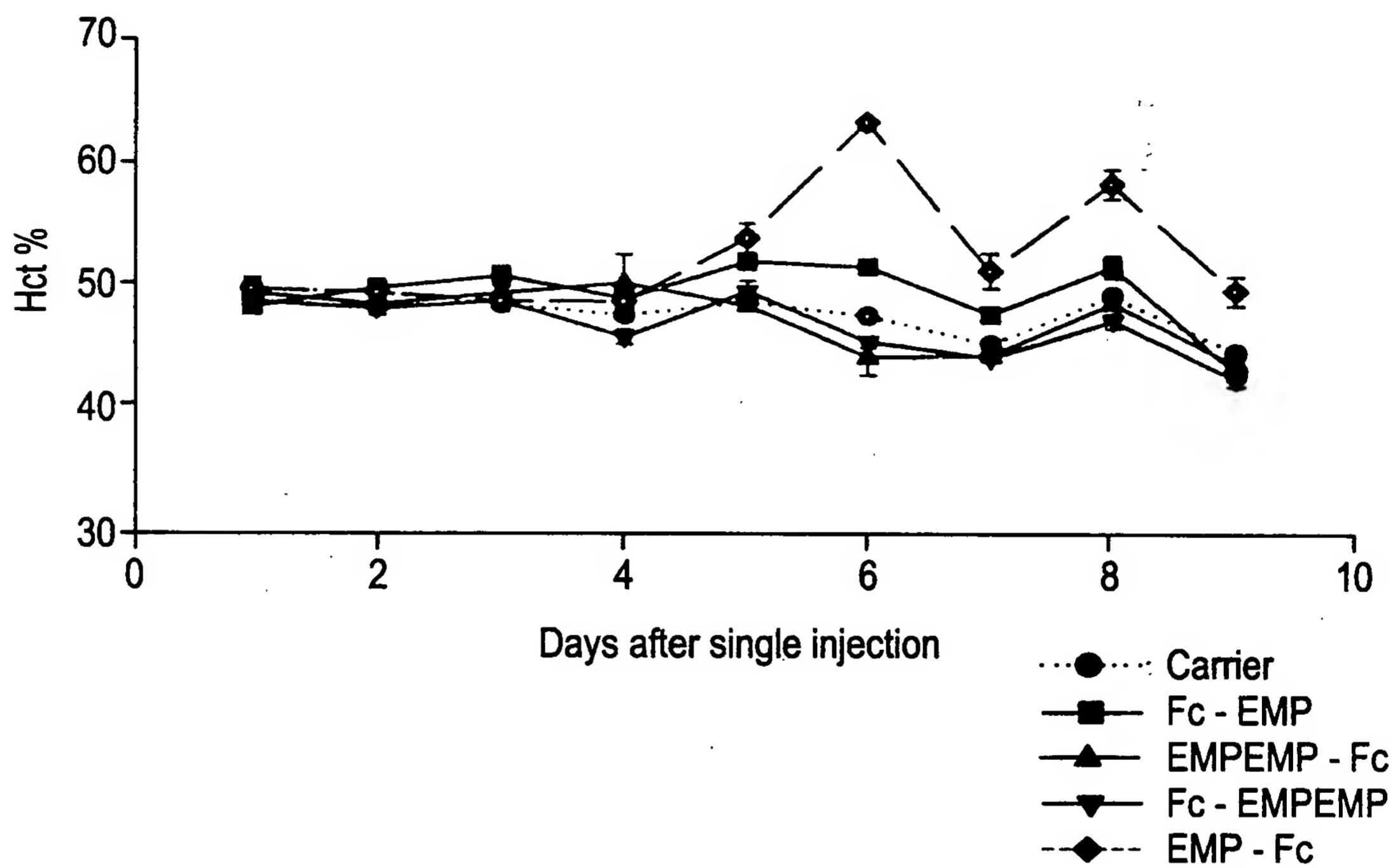


FIG.18B - 1

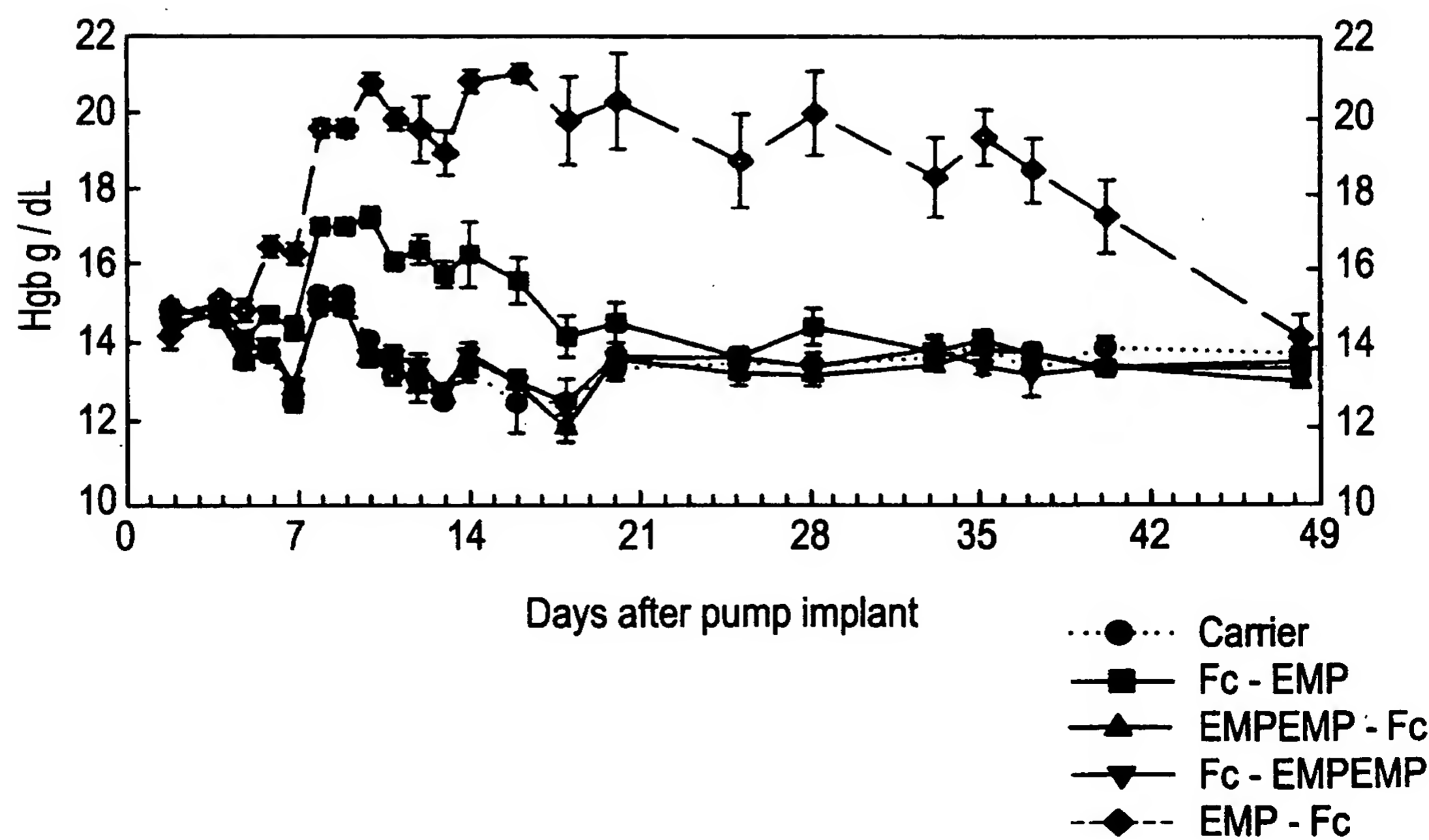


FIG.18B - 2

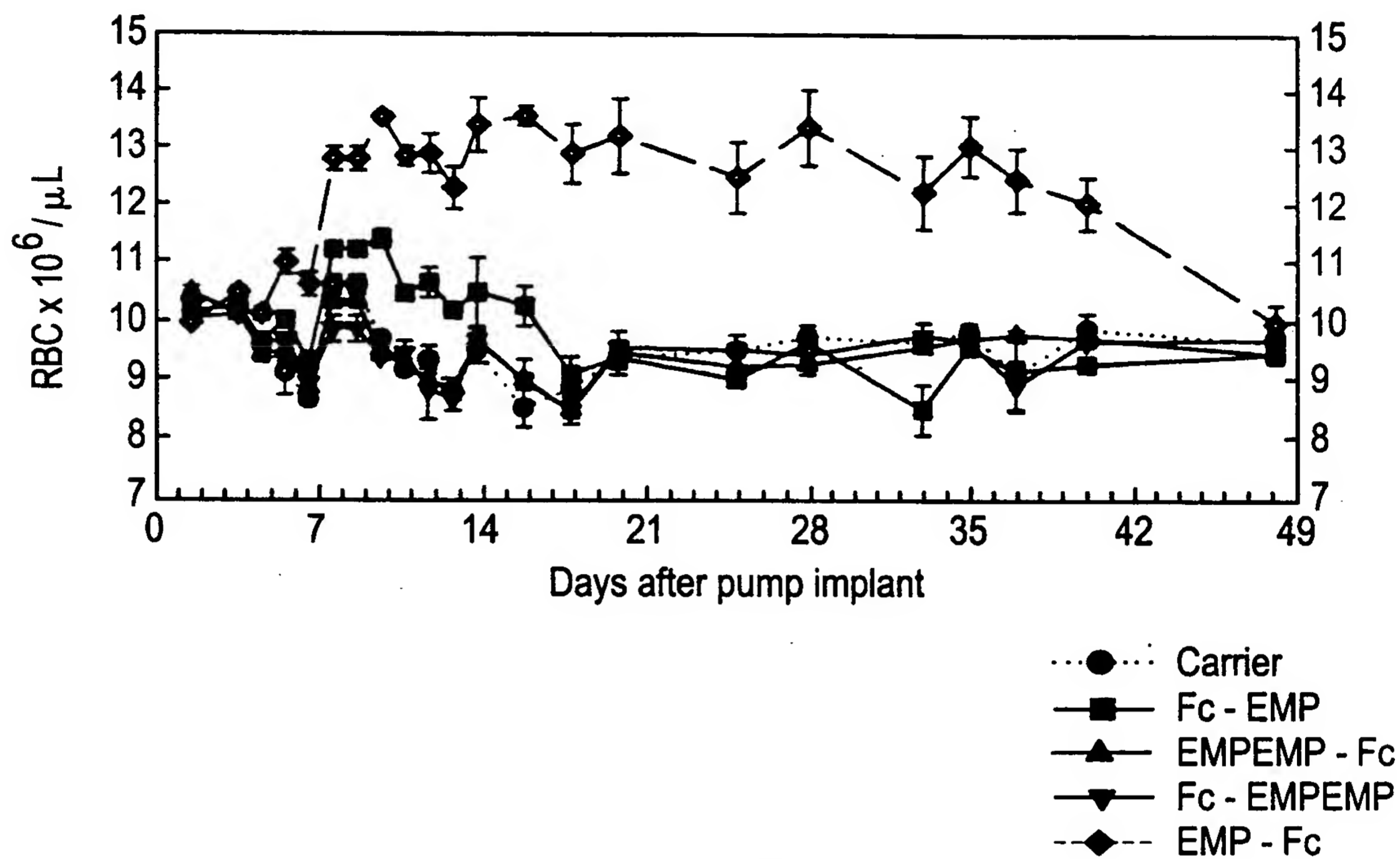


FIG.18B - 3

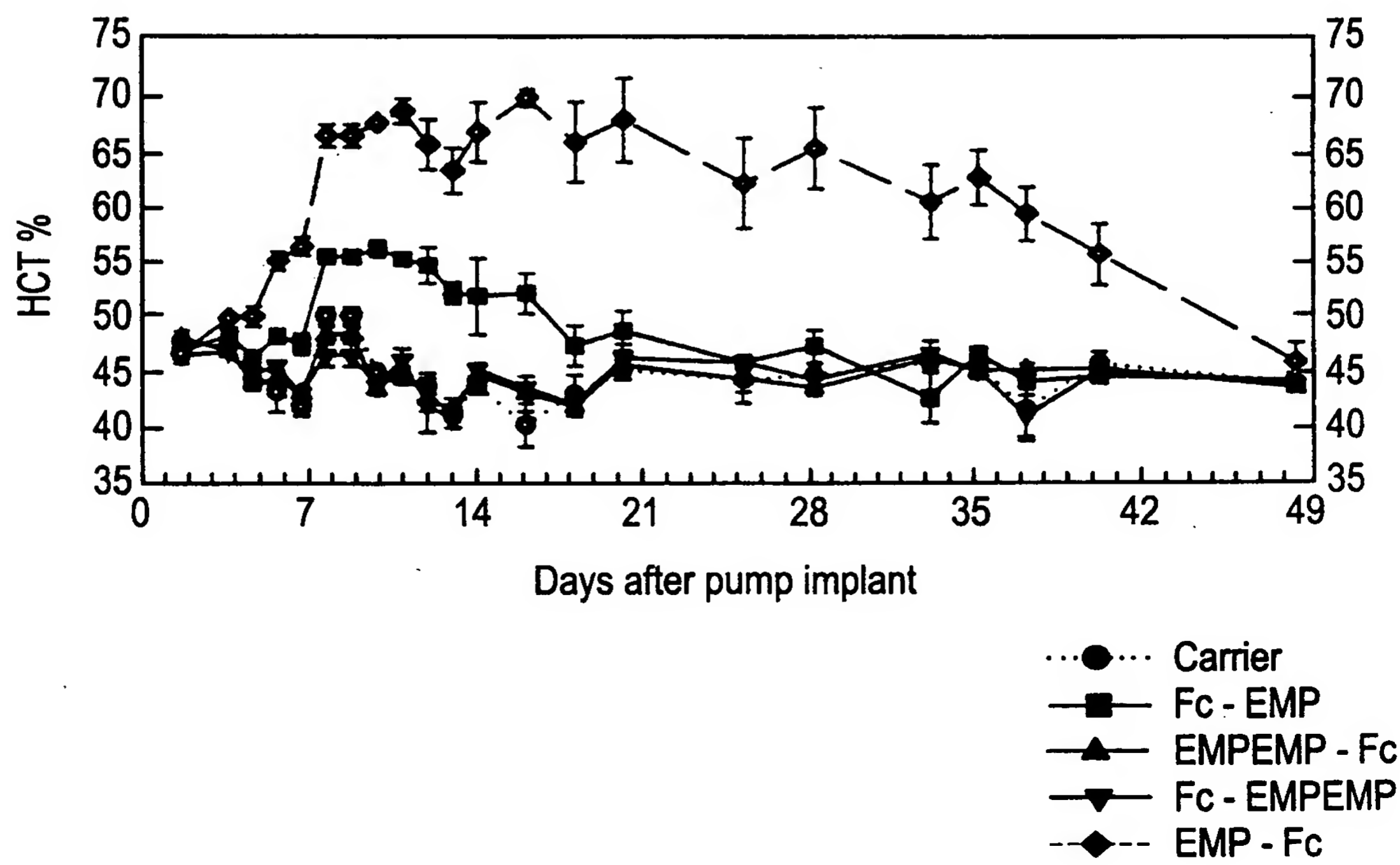


FIG. 19A

NdeI
|
1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCCTGGGGGGACCG 60
-----+-----+-----+-----+-----+-----+-----+
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC
a M D K T H T C P P C P A P E L L G G P -
61 TCAGTCTTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
-----+-----+-----+-----+-----+-----+-----+
AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
-----+-----+-----+-----+-----+-----+-----+
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
-----+-----+-----+-----+-----+-----+-----+
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCTG
a V D G V E V H N A K T K P R E E Q Y N S -
241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
-----+-----+-----+-----+-----+-----+-----+
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTCCTC
a T Y R V V S V L T V L H Q D W L N G K E -
301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
-----+-----+-----+-----+-----+-----+-----+
ATGTTACAGTTCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K -
361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
-----+-----+-----+-----+-----+-----+-----+
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
-----+-----+-----+-----+-----+-----+-----+
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTG 540
-----+-----+-----+-----+-----+-----+-----+
CACCTCACCTCTCTGTTACCCGTGGCCTCTTGTGATGTTCTGGTGCGGAGGGGCACGAC
a V E W E S N G Q P E N N Y K T T P P V L -
541 GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
-----+-----+-----+-----+-----+-----+-----+
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC
a D S D G S F F L Y S K L T V D K S R W Q -

FIG. 19B

```
601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
-----+-----+-----+-----+-----+-----+-----+
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a   Q   G   N   V   F   S   C   S   V   M   H   E   A   L   H   N   H   Y   T   Q   -

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTGACTTCCTGCCGCACTAC 720
-----+-----+-----+-----+-----+-----+-----+
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCACTGAAGGACGGCGTGATG

a   K   S   L   S   L   S   P   G   K   G   G   G   G   G   D   F   L   P   H   Y   -

                                     BamHI
                                     |
721 AAAAACACCTCTCTGGGTCACCGTCCGTAATGGATCC 757
-----+-----+-----+-----+-----+-----+
TTTTTGTGGAGAGACCCAGTGGCAGGCATTACCTAGG

a   K   N   T   S   L   G   H   R   P   *
```

FIG. 20A

NdeI
|
1 CATATGGACTTCCTGCCGCACTACAAAAACACCTCTCTGGGTACCGTCCGGGTGGAGGC 60
-----+-----+-----+-----+-----+-----+-----+
GTATACCTGAAGGACGGCGTGATGTTTTGTGGAGAGACCCAGTGGCAGGCCACCTCCG
a M D F L P H Y K N T S L G H R P G G G -
61 GGTGGGGACAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCG 120
-----+-----+-----+-----+-----+-----+-----+
CCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGC
a G G D K T H T C P P C P A P E L L G G P -
121 TCAGTTTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 180
-----+-----+-----+-----+-----+-----+-----+
AGTCAAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
181 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 240
-----+-----+-----+-----+-----+-----+-----+
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
241 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 300
-----+-----+-----+-----+-----+-----+-----+
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG
a V D G V E V H N A K T K P R E E Q Y N S -
301 ACGTACCGTGTGGTCAGCGTCCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 360
-----+-----+-----+-----+-----+-----+-----+
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC
a T Y R V V S V L T V L H Q D W L N G K E -
361 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 420
-----+-----+-----+-----+-----+-----+-----+
ATGTTACAGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K -
421 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 480
-----+-----+-----+-----+-----+-----+-----+
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
481 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 540
-----+-----+-----+-----+-----+-----+-----+
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
541 GTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGTGCTG 600
-----+-----+-----+-----+-----+-----+-----+
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGGGAGGGGCACGAC
a V E W E S N G Q P E N N Y K T T P P V L -

FIG. 20B

601 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 660
-----+-----+-----+-----+-----+-----+-----+
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC
a D S D G S F F L Y S K L T V D K S R W Q -
661 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 720
-----+-----+-----+-----+-----+-----+-----+
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC
a Q G N V F S C S V M H E A L H N H Y T Q -

BamHI
|
721 AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCCGCGG 761
-----+-----+-----+-----+-----+-----+-----+
TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGGCGCC
a K S L S L S P G K *

FIG. 21A

NdeI
|
CATATGGACAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCCTGGGGGGACCG
1 -----+-----+-----+-----+-----+-----+-----+ 60
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC

a M D K T H T C P P C P A P E L L G G P -

TCAGTCTTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
61 -----+-----+-----+-----+-----+-----+ 120
AGTCAGAAGGAGAAGGGGGGTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
121 -----+-----+-----+-----+-----+-----+ 180
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
181 -----+-----+-----+-----+-----+-----+ 240
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG

a V D G V E V H N A K T K P R E E Q Y N S -

ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
241 -----+-----+-----+-----+-----+-----+ 300
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC

a T Y R V V S V L T V L H Q D W L N G K E -

TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
301 -----+-----+-----+-----+-----+-----+ 360
ATGTTACAGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -

GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
361 -----+-----+-----+-----+-----+-----+ 420
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
421 -----+-----+-----+-----+-----+-----+ 480
TGGTTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

GTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGTGCTG
481 -----+-----+-----+-----+-----+-----+ 540
CACCTCACCCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC

a V E W E S N G Q P E N N Y K T T P P V L -

GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
541 -----+-----+-----+-----+-----+-----+ 600
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a D S D G S F F L Y S K L T V D K S R W Q -

FIG. 21B

```
601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 660
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a      Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  -

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTTCGAATGGACCCCGGGT
-----+-----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAAAGCTTACCTGGGGCCCA

a      K  S  L  S  L  S  P  G  K  G  G  G  G  G  F  E  W  T  P  G  -

                                     BamHI
                                     |
721 TACTGGCAGCCGTACGCTCTGCCGCTGTAATGGATCCCTCGAG
-----+-----+-----+-----+-----+ 763
ATGACCGTCGGCATGCGAGACGGCGACATTACCTAGGGAGCTC

a      Y  W  Q  P  Y  A  L  P  L  *
```

FIG. 22A

NdeI
|
CATATGTTCTGAATGGACCCCGGGTTACTGGCAGCCGTACGCTCTGCCGCTGGGTGGAGGC
1 -----+-----+-----+-----+-----+-----+-----+ 60
GTATACAAGCTTACCTGGGGCCCAATGACCGTCGGCATGCGAGACGGCGACCCACCTCCG
a M F E W T P G Y W Q P Y A L P L G G G -
GGTGGGGACAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCG
61 -----+-----+-----+-----+-----+-----+-----+ 120
CCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCTGGC
a G G D K T H T C P P C P A P E L L G G P -
TCAGTTTTCTCTTCCCCC AAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
121 -----+-----+-----+-----+-----+-----+-----+ 180
AGTCAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
181 -----+-----+-----+-----+-----+-----+-----+ 240
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
241 -----+-----+-----+-----+-----+-----+-----+ 300
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCTG
a V D G V E V H N A K T K P R E E Q Y N S -
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
301 -----+-----+-----+-----+-----+-----+-----+ 360
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTCCTC
a T Y R V V S V L T V L H Q D W L N G K E -
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
361 -----+-----+-----+-----+-----+-----+-----+ 420
ATGTTTACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K -
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
421 -----+-----+-----+-----+-----+-----+-----+ 480
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
481 -----+-----+-----+-----+-----+-----+-----+ 540
TGGTTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTG
541 -----+-----+-----+-----+-----+-----+-----+ 600
CACCTCACCTCTCGTTACCCGTGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC
a V E W E S N G Q P E N N Y K T T P P V L -

FIG. 22B

601 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 660
-----+-----+-----+-----+-----+-----+-----+
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC
a D S D G S F F L Y S K L T V D K S R W Q -
661 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 720
-----+-----+-----+-----+-----+-----+-----+
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC
a Q G N V F S C S V M H E A L H N H Y T Q -
BamHI
|
721 AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC 757
-----+-----+-----+-----+-----+
TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG
a K S L S L S P G K *

FIG. 23A

NdeI
|
CATATGGACAAAACTCACACATGTCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCG
1 -----+-----+-----+-----+-----+-----+-----+ 60
GTATACCTGTTTGTGAGTGTGTACAGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGC
a M D K T H T C P P C P A P E L L G G P -
TCAGTTTTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
61 -----+-----+-----+-----+-----+-----+-----+ 120
AGTCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
121 -----+-----+-----+-----+-----+-----+-----+ 180
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
181 -----+-----+-----+-----+-----+-----+-----+ 240
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCTG
a V D G V E V H N A K T K P R E E Q Y N S -
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
241 -----+-----+-----+-----+-----+-----+-----+ 300
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC
a T Y R V V S V L T V L H Q D W L N G K E -
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
301 -----+-----+-----+-----+-----+-----+-----+ 360
ATGTTACAGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K -
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
361 -----+-----+-----+-----+-----+-----+-----+ 420
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
421 -----+-----+-----+-----+-----+-----+-----+ 480
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTG
481 -----+-----+-----+-----+-----+-----+-----+ 540
CACCTCACCCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC
a V E W E S N G Q P E N N Y K T T P P V L -
GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
541 -----+-----+-----+-----+-----+-----+-----+ 600
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC
a D S D G S F F L Y S K L T V D K S R W Q -

FIG. 23B

601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
-----+-----+-----+-----+-----+-----+
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC
a Q G N V F S C S V M H E A L H N H Y T Q -
AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGTGGTGGTGGTGGTGAACCGAACTGTGAC
661 -----+-----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCACCACCACCACAACCTTGGCTTGACACTG
a K S L S L S P G K G G G G G V E P N C D -
BamHI
|
721 ATCCATGTTATGTGGGAATGGGAATGTTTTGAACGTCTGTAACCTCGAGGATCC 773
-----+-----+-----+-----+-----+-----+
TAGGTACAATACACCCTTACCCTTACAAAACCTGCAGACATTGAGCTCCTAGG
a I H V M W E W E C F E R L *

FIG. 24A

NdeI
|
CATATGGTTGAACCGAACTGTGACATCCATGTTATGTGGGAATGGGAATGTTTTGAACGT
1 -----+-----+-----+-----+-----+-----+-----+ 60
GTATACCAACTTGGCTTGACACTGTAGGTACAATACACCCTTACCCTTACAAAACCTTGCA
a M V E P N C D I H V M W E W E C F E R -
CTGGGTGGTGGTGGTGGTGACAAAACCTCACACATGTCCACCGTGCCCAGCACCTGAACTC
61 -----+-----+-----+-----+-----+-----+-----+ 120
GACCCACCACCACCACCCTGTTTTGAGTGTGTACAGGTGGCACGGGTCGTGGACTTGAG
a L G G G G G D K T H T C P P C P A P E L -
CTGGGGGGACCGTCAGTTTTCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCC
121 -----+-----+-----+-----+-----+-----+-----+ 180
GACCCCCCTGGCAGTCAAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGG
a L G G P S V F L F P P K P K D T L M I S -
CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG
181 -----+-----+-----+-----+-----+-----+-----+ 240
GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC
a R T P E V T C V V V D V S H E D P E V K -
TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG
241 -----+-----+-----+-----+-----+-----+-----+ 300
AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTC
a F N W Y V D G V E V H N A K T K P R E E -
CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
301 -----+-----+-----+-----+-----+-----+-----+ 360
GTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGAC
a Q Y N S T Y R V V S V L T V L H Q D W L -
AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA
361 -----+-----+-----+-----+-----+-----+-----+ 420
TTACCGTTCCTCATGTTACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT
a N G K E Y K C K V S N K A L P A P I E K -
ACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC
421 -----+-----+-----+-----+-----+-----+-----+ 480
TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGG
a T I S K A K G Q P R E P Q V Y T L P P S -
CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
481 -----+-----+-----+-----+-----+-----+-----+ 540
GCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGG
a R D E L T K N Q V S L T C L V K G F Y P -
AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACG
541 -----+-----+-----+-----+-----+-----+-----+ 600
TCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGC
a S D I A V E W E S N G Q P E N N Y K T T -

FIG. 24B

601 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 660
-----+-----+-----+-----+-----+-----+-----+
GGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTC
a P P V L D S D G S F F L Y S K L T V D K -
661 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 720
-----+-----+-----+-----+-----+-----+-----+
TCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG
a S R W Q Q G N V F S C S V M H E A L H N -
BamHI
|
721 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAACTCGAGGATCC 773
-----+-----+-----+-----+-----+-----+-----+
GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTGAGCTCCTAGG
a H Y T Q K S L S L S P G K *

FIG. 25A

NdeI
|
1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCCTGGGGGGACCG
-----+-----+-----+-----+-----+-----+-----+ 60
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC

a M D K T H T C P P C P A P E L L G G P -

61 TCAGTCTTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
-----+-----+-----+-----+-----+-----+ 120
AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
-----+-----+-----+-----+-----+ 180
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
-----+-----+-----+-----+-----+ 240
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG

a V D G V E V H N A K T K P R E E Q Y N S -

241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
-----+-----+-----+-----+-----+ 300
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC

a T Y R V V S V L T V L H Q D W L N G K E -

301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
-----+-----+-----+-----+-----+ 360
ATGTTACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -

361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
-----+-----+-----+-----+-----+ 420
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
-----+-----+-----+-----+-----+ 480
TGGTTCCTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTG
-----+-----+-----+-----+-----+ 540
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC

a V E W E S N G Q P E N N Y K T T P P V L -

541 GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
-----+-----+-----+-----+-----+ 600
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a D S D G S F F L Y S K L T V D K S R W Q -

FIG. 25B

601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
-----+-----+-----+-----+-----+-----+
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC
a Q G N V F S C S V M H E A L H N H Y T Q -
AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTGCACCACCCACTGGGGT
661 -----+-----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAACGTGGTGGGTGACCCCA
A K S L S L S P G K G G G G G C T T H W G -
BamHI
|
TTCACCCTGTGCTAATGGATCCCTCGAG
721 -----+-----+-----+-----+-----+ 748
AAGTGGGACACGATTACCTAGGGAGCTC
a F T L C *

FIG. 26A

NdeI
|
CATATGTGCACCACCCACTGGGGTTTCACCCTGTGCGGTGGAGGCGGTGGGGACAAAGGT
1+.....+.....+.....+.....+.....+.....+ 60
GTATACACGTGGTGGGTGACCCCAAAGTGGGACACGCCACCTCCGCCACCCCTGTTTCCA

a M C T T H W G F T L C G G G G G D K G -

61 GGAGGCGGTGGGGACAAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGG
.....+.....+.....+.....+.....+.....+.....+ 120
CCTCCGCCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCC

a G G G G D K T H T C P P C P A P E L L G -

121 GGACCGTCAGTTTTCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACC
.....+.....+.....+.....+.....+.....+.....+ 180
CCTGGCAGTCAAAGGAGAAGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGG

a G P S V F L F P P K P K D T L M I S R T -

181 CCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
.....+.....+.....+.....+.....+.....+.....+ 240
GGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTG

a P E V T C V V V D V S H E D P E V K F N -

241 TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTAC
.....+.....+.....+.....+.....+.....+.....+ 300
ACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATG

a W Y V D G V E V H N A K T K P R E E Q Y -

301 AACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGC
.....+.....+.....+.....+.....+.....+.....+ 360
TTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCG

a N S T Y R V V S V L T V L H Q D W L N G -

361 AAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATC
.....+.....+.....+.....+.....+.....+.....+ 420
TTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAG

a K E Y K C K V S N K A L P A P I E K T I -

421 TCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAT
.....+.....+.....+.....+.....+.....+.....+ 480
AGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTA

a S K A K G Q P R E P Q V Y T L P P S R D -

481 GAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGAC
.....+.....+.....+.....+.....+.....+.....+ 540
CTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTTCGCTG

a E L T K N Q V S L T C L V K G F Y P S D -

541 ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCC
.....+.....+.....+.....+.....+.....+.....+ 600
TAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGC GGAGGG

a I A V E W E S N G Q P E N N Y K T T P P -

BamHI